

***Remarks***

Reconsideration of this Application is respectfully requested.

The above amendments do not add new matter. The amendments correct a formal matter without changing the scope of the claims. Specifically, the amendments are in response to the Office Communication, dated October 22, 2002, requesting the insertion of SEQ ID numbers for reference peptides found in the tables located on pages 33-179 of the specification. Applicants point out that all of the peptide sequences listed in Tables 1-3 and 5-6 are sequences contained within the full-length C35 polypeptide sequence of SEQ ID NO: 2 at the positions noted. As such, they do not require their own SEQ ID NOS. Paragraph 87 has been amended to further clarify this. Table 4, in addition to listing peptide sequences contained in SEQ ID NO: 2, also contains "modified" C35 peptide sequences containing amino acid substitutions. The modified sequences correspond to SEQ ID NOS: 85-147. Table 4 has been amended to specifically associate the SEQ ID NOS with the corresponding sequences. These changes are believed to introduce no new matter, and their entry is respectfully requested.

***Conclusion***

Applicants believe that a full and complete reply has been made to the outstanding Office Communication. If the Examiner believes, for any reason, that

personal communication will expedite prosecution of this application, the Examiner is invited to telephone the undersigned at the number provided.

Prompt and favorable consideration of this Amendment and Reply is respectfully requested.

Respectfully submitted,

STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.



Timothy J. Shea, Jr.  
Attorney for Applicant  
Registration No. 41,306

Date: 11/22/02

1100 New York Avenue, N.W.  
Suite 600  
Washington, D.C. 20005-3934  
(202) 371-2600

**Version with markings to show changes made**

--A number of computer algorithms have been described for identification of peptides in a larger protein that may satisfy the requirements of peptide binding motifs for specific MHC class I or MHC class II molecules. Because of the extensive polymorphism of MHC molecules, different peptides will often bind to different MHC molecules. Tables 1-3 list C35 peptides predicted to be MHC binding peptides using three different algorithms. Specifically, Tables 1 and 5 list C35 HLA Class I and II epitopes predicted using the rules found at the SYFPEITHI website ([wysiwyg://35/http://134.2.96.221/scripts/hlaserver.dll/EpPredict.htm](http://35/http://134.2.96.221/scripts/hlaserver.dll/EpPredict.htm)) and are based on the book "MHC Ligands and Peptide Motifs" by Rammensee, H.G., Bachmann, J. and Stevanovic, S. (Chapman & Hall, New York 1997). Table 2 lists predicted MHC binding peptides derived from the C35 sequence using the NIH BIMAS program available on the web ([http://bimas.dcrt.nih.gov/cgi-bin/molbio/ken\\_parker\\_comboform](http://bimas.dcrt.nih.gov/cgi-bin/molbio/ken_parker_comboform)). Finally, Tables 3 and 6 list predicted C35 peptides identified by the Tepitope program, a program for prediction of peptides that may bind to multiple different MHC class II molecules. Using Tepitope, four C35 peptides were identified as likely candidates for binding to a variety of HLA class II molecules. These peptides are, in general, longer than those binding to HLA class I and more degenerate in terms of binding to multiple HLA class II molecules. Unless expressly noted otherwise, all peptide sequences listed in Tables 1-6 refer to C35 peptide sequences appearing in SEQ ID NO:2 at the amino acid positions noted.--

**TABLE 4**  
**Modifications that Enhance HLA Class I Binding**

(Unless otherwise indicated, examples apply to peptides of 9 amino acids; for 10-mers the amino acid at position 5 is disregarded and the resultant 9-mer is evaluated ([http://bimas.dcrt.nih.gov/cgi-bin/molbio/hla\\_coefficient](http://bimas.dcrt.nih.gov/cgi-bin/molbio/hla_coefficient) viewing\_page. The modifications listed below are provided by way of example based on current data in existing databases and are not intended in any way to be an inclusive list of all potential alterations of peptides binding all potential HLA molecules, both known and unknown to date.)

**HLA A\*0101**

Any altered peptide that has S or T at position 2

Any altered peptide that has D or E at position 3

Any altered peptide that has P at position 4

Any altered peptide that has A, F, I, L, M, P, V, or Y at position 7

Any altered peptide that has F, K, R, or Y at anchor position 9

Any altered peptide where deleterious residues at the following positions are replaced:

P1: P

P2: D, E, F, G, H, K, M, N, P, Q, R, W, Y

P3: E, K, R, W

P4: K, R

P7: D, E, G, R

P9: D, E, P

**HLA A\*0201**

Any altered peptide that has F, I, K, L, M, V, W, or Y at position 1

Any altered peptide that has I, L, M, Q, or V at anchor position 2

Any altered peptide that has F, L, M, W, or Y at position 3

Any altered peptide that has D or E at position 4

Any altered peptide that has F at position 5

Any altered peptide that has F, I, L, M, V, W or Y at auxiliary anchor position 6

Any altered peptide that has F, or W at position 7

Any altered peptide that has F, W, or Y at position 8

Any altered peptide that has I, L, T or V at anchor position 9

Any altered peptide where deleterious residues at the following positions are replaced:

P1: D, E, H, P  
P2: C, F, H, K, N, P, R, S, W, Y  
P3: D, E, K, R  
P7: D, E, G, R  
P8: I, V  
P9: D, E, F, G, H, K, N, P, Q, R, S, W, Y

**HLA-A\*0205**

Any altered peptide that has F, I, K, L, M, V, W, or Y at position 1  
Any altered peptide that has E, I, L, M, Q, or V at anchor position 2  
Any altered peptide that has F, L, M, W, or Y at position 3  
Any altered peptide that has D or E at position 4  
Any altered peptide that has F, Y at position 5  
Any altered peptide that has F, I, L, M, V, W or Y at auxiliary anchor position 6  
Any altered peptide that has F, or W at position 7  
Any altered peptide that has F, W, or Y at position 8  
Any altered peptide that has I, L, T or V at anchor position 9

Any altered peptide where deleterious residues at the following positions are replaced:

P1: D, E, P  
P2: C, D, F, G, H, K, N, P, R, S, W, Y  
P3: D, E, K, R  
P7: D, E, R  
P9: D, E, F, G, H, K, N, P, Q, R, S, W, Y

**HLA-A\*03**

Any altered peptide that has G or K at position 1  
Any altered peptide that has I, L, M, Q, T or V at anchor position 2  
Any altered peptide that has F, I, L, M, V, W, or Y at position 3  
Any altered peptide that has E, G or P at position 4  
Any altered peptide that has F, I, P, V, W, Y at position 5  
Any altered peptide that has F, I, L, M, or V at position 6  
Any altered peptide that has F, I, L, M, W, or Y at position 7

Any altered peptide that has F, I, K, L, Q or Y at anchor position 9

Any altered peptide where deleterious residues at the following positions are replaced:

P1: D, E, P

P2: D, E, F, G, H, K, N, R, S, W, Y

P7: G, K, R

P9: D, E, G, H, N, P, Q, S, T

#### **HLA-A\*1101**

Any altered peptide that has G, K or R at position 1

Any altered peptide that has I, L, M, Q, T, V, Y at anchor position 2

Any altered peptide that has F, I, L, M, V, W, Y at position 3

Any altered peptide that has F, I, L, M, W or Y at position 7

Any altered peptide that has K or R at anchor position 9

Any altered peptide where deleterious residues at the following positions are replaced:

P1: D, E, P

P2: D, E, G, H, K, N, R, S, W

P7: K, R

P9: C, D, E, G, N, P, Q, S, T

#### **HLA-A24**

Any altered peptide that has K or R at position 1

Any altered peptide that has F or Y at anchor position 2

Any altered peptide that has E, I, L, M, N, P, Q, or V at position 3

Any altered peptide that has D, E, or P at position 4

Any altered peptide that has I, L, or V at position 5

Any altered peptide that has F at position 6

Any altered peptide that has N or Q at position 7

Any altered peptide that has E or K at position 8

Any altered peptide that has F, I, L, or M at anchor position 9

Any altered peptide where deleterious residues at the following positions are replaced:

P1: P

P2: D, E, H, K, R

P9: D, E, G, H, K, P, Q, R

**HLA-A\*3101**

Any altered peptide that has K or R at position 1  
Any altered peptide that has F, I, L, M, Q, T, V, or Y at anchor position 2  
Any altered peptide that has F, I, L, M, V W, or Y at position 3  
Any altered peptide that has F, I, L, M, or V at position 6  
Any altered peptide that has F, I, L, M, W, or Y at position 7  
Any altered peptide that has K or R at anchor position 9  
Any altered peptide where deleterious residues at the following positions are replaced:  
P1: D, E, P  
P2: D, E, G, H, K, N, R, S  
P7: K, R  
P9: C, G, N, P, Q, S, T

**HLA-A\*3302**

Any altered peptide that has D or E at position 1  
Any altered peptide that has I, L, M, S, V or Y at anchor position 2  
Any altered peptide that has R at anchor position 9  
Any altered peptide where deleterious residues at the following positions are replaced:  
P1: K, P, R  
P2: D, E, K, R  
P9: D, E, F, G, N, P, W, Y

**HLA-B7**

Any altered peptide that has A at position 1  
Any altered peptide that has A, P or V at anchor position 2  
Any altered peptide that has M or R at position 3  
Any altered peptide that has P at position 5  
Any altered peptide that has R at position 6  
Any altered peptide that has I, L, M or V at anchor position 9

Any altered peptide where deleterious residues at the following positions are replaced:

P1: P  
P2: D, E, F, H, K, R, W, Y  
P3: D, E  
P9: D, E, F, G, H, K, N, P, Q, R, S, W, Y

#### **HLA-B8**

Any altered peptide that has D or E at position 1  
Any altered peptide that has A, C, L, or P at anchor position 2  
Any altered peptide that has K or R at position 3  
Any altered peptide that has D or E at position 4  
Any altered peptide that has K or R at position 5  
Any altered peptide that has I, L, M, or V at anchor position 9

Any altered peptide where deleterious residues at the following positions are replaced:

P1: K, P, R  
P2: D, E, F, G, H, K, Q, R, W, or Y  
P3: D, E  
P5: D, E  
P9: D, E, F, G, H, K, N, P, Q, R, S, W, Y

#### **HLA-B8 (8-mer peptides)**

Any altered peptide that has D or E at position 1  
Any altered peptide that has A, C, L, or P at anchor position 2  
Any altered peptide that has K or R at position 3  
Any altered peptide that has D or E at position 4  
Any altered peptide that has K or R at position 5  
Any altered peptide that has I, L, M, or V at anchor position 8

Any altered peptide where deleterious residues at the following positions are replaced:

P1: K, P, R  
P2: D, E, F, G, H, K, Q, R, W, or Y  
P3: D, E  
P5: D, E  
P8: D, E, F, G, H, K, N, P, Q, R, S, W, Y

**HLA-B14**

Any altered peptide that has D or E at position 1

Any altered peptide that has K or R at anchor position 2

Any altered peptide that has F, I, L, M, P, V, W, Y at position 3

Any altered peptide that has H or R at position 5

Any altered peptide that has I, L, M, R, or V at position 6

Any altered peptide that has T at position 7

Any altered peptide that has I, L, M, or V at anchor position 9

Any altered peptide where deleterious residues at the following positions are replaced:

P1: P

P2: D, E, F, W, or Y

P3: E, R

P5: E, W, Y

P9: D, E, G, H, K, N, P, Q, R

**HLA-B\*2702**

Any altered peptide that has K or R at position 1

Any altered peptide that has E, L, M, N, Q or R at anchor position 2

Any altered peptide that has F, W, or Y at position 3

Any altered peptide that has F, I, L, W or Y at anchor position 9

Any altered peptide where deleterious residues at the following positions are replaced:

P1: D, E, P

P2: D, F, G, H, K, W, or Y

P7: K

P9: D, E, G, K, N, P, Q, R, S

**HLA-B27\*05 (8-mer peptides)**

Any altered peptide that has K or R at position 1

Any altered peptide that has E, L, M, N, Q or R at anchor position 2

Any altered peptide that has F, W, or Y at position 3

Any altered peptide that has F, I, K, L, M, R, V or Y at anchor position 8

Any altered peptide where deleterious residues at the following positions are replaced:

P1: D, E, P  
P2: D, F, G, H, K, W, or Y  
P7: K  
P9: D, E, G, K, N, P, Q, R, S

**HLA-B\*3501 (8-mer peptides)**

Any altered peptide that has K or R at position 1  
Any altered peptide that has A, P, or S at anchor position 2  
Any altered peptide that has K or R at position 3  
Any altered peptide that has D or E at position 4  
Any altered peptide that has D or E at position 5  
Any altered peptide that has F, I, L, M, V, W or Y at anchor position 8

Any altered peptide where deleterious residues at the following positions are replaced:

P1: P  
P2: D, E, F, H, K, R, W, Y  
P3: D, E  
P8: D, E, F, G, H, K, P, Q, R

**HLA-B\*3701**

Any altered peptide that has D or E at anchor position 2  
Any altered peptide that has I or V at position 5  
Any altered peptide that has F, L, or M at position 8  
Any altered peptide that has F, I, L, M, V or Y at anchor position 9

Any altered peptide where deleterious residues at the following positions are replaced:

P1: P  
P9: D, E, G, H, K, P, Q, R

**HLA-B\*3801**

Any altered peptide that has F, H, P, W or Y at anchor position 2  
Any altered peptide that has D or E at position 3  
Any altered peptide that has D, E, or G at position 4  
Any altered peptide that has A, I, L, M, or V at position 5

Any altered peptide that has K or Y at position 8

Any altered peptide that has F, I, L, M, or V at anchor position 9

Any altered peptide where deleterious residues at the following positions are replaced:

P1: P

P2: D, E, K, R

P3: K, R

P9: D, E, G, H, K, P, Q, R

#### **HLA-B\*3901 (8-mer peptides)**

Any altered peptide that has H or R at anchor position 2

Any altered peptide that has D, E, F, I, L, M, V, W, or W at position 3

Any altered peptide that has D or E at position 4

Any altered peptide that has I, L, M, or V at position 6

Any altered peptide that has I, L, M or V at anchor position 8

Any altered peptide where deleterious residues at the following positions are replaced:

P1: P

P2: D, E

P3: K, R

P6: D, E, K, R

P8: D, E, G, H, K, P, Q, R

#### **HLA-B\*3902**

Any altered peptide that has K or Q at anchor position 2

Any altered peptide that has F, I, L, M, V, W, or Y at position 5

Any altered peptide that has F, L, or M at anchor position 9

Any altered peptide where deleterious residues at the following positions are replaced:

P1: P

P2: D, E

P3: K, R

P9: D, E, G, H, K, P, Q, R

#### **HLA-B40**

Any altered peptide that has A or G at position 1

Any altered peptide that has D or E at anchor position 2

Any altered peptide that has A, F, I, L, M, V, W, or Y at position 3

Any altered peptide that has P at position 4

Any altered peptide that has P at position 5

Any altered peptide that has A, L, M, or W at anchor position 9

Any altered peptide where deleterious residues at the following positions are replaced:

P1: P

P2: F, H, I, K, L, M, Q, R, V, W, or Y

P3: D, E, K, R

P9: D, E, G, H, K, N, P, Q, R

#### **HLA-B44\*03**

Any altered peptide that has A, D, or S at position 1

Any altered peptide that has D or E at anchor position 2

Any altered peptide that has A, I, L, M, or V at position 3

Any altered peptide that has F, I, or P at position 4

Any altered peptide that has A, K, or V at position 5

Any altered peptide that has A, L, T, or V at position 6

Any altered peptide that has F, K, or T at position 7

Any altered peptide that has K at position 8

Any altered peptide that has F, W or Y at anchor position 9

Any altered peptide where deleterious residues at the following positions are replaced:

P1: P

P2: F, H, I, K, L, M, Q, R, V, W, Y

P9: D, E, G, H, K, N, P, Q, R

#### **HLA-B\*5101 (8-mer peptides)**

Any altered peptide that has D, E, F, I, L, M, V, or Y at position 1

Any altered peptide that has A, G or P at anchor position 2

Any altered peptide that has F, W or Y at position 3

Any altered peptide that has D, E, G, I, K, or V at position 4

Any altered peptide that has A, G, I, S, T, or V at position 5

Any altered peptide that has I, K, L, N, or Q at position 6

Any altered peptide that has D, K, Q, or R at position 7

Any altered peptide that has I, L, M, or V at anchor position 8

Any altered peptide where deleterious residues at the following positions are replaced:

P1: K, P, R

P2: D, E, H, K

P8: D, E, F, G, H, K, N, P, Q, R, S, W, Y

#### **HLA-B\*5102**

Any altered peptide that has F or Y at position 1

Any altered peptide that has A, G, or P at anchor position 2

Any altered peptide that has F, I, L, V, W, or Y at position 3

Any altered peptide that has E, G, H, K, L, N, Q, R, or T at position 4

Any altered peptide that has G, N, Q, T, or V at position 5

Any altered peptide that has I, N, Q, or T at position 6

Any altered peptide that has E, K, Q, or R at position 7

Any altered peptide that has K, R, T, or Y at position 8

Any altered peptide that has I, L, M, or V at anchor position 9

Any altered peptide where deleterious residues at the following positions are replaced:

P1: P

P2: D, E, H, K, R

P3: D, E, K, R

P9: D, E, F, G, H, K, N, P, Q, R, S, W, Y

#### **HLA-B\*5102 (8-mer peptides)**

Any altered peptide that has F or Y at position 1

Any altered peptide that has A, G, or P at anchor position 2

Any altered peptide that has F, I, L, V, W, or Y at position 3

Any altered peptide that has E, G, H, K, L, V, W, or Y at position 4

Any altered peptide that has G, N, Q, T, V at position 5

Any altered peptide that has I, N, or Q at position 6

Any altered peptide that has Q, or R at position 7

Any altered peptide that has I, L, M, or V at position 8

Any altered peptide where deleterious residues at the following positions are replaced:

P1: P

P2: D, E, H, K, R

P3: D, E, K, R

P8: D, E, F, G, H, K, N, P, Q, R, S, W, Y

#### **HLA-B\*5103**

Any altered peptide that has D, T, or V at position 1

Any altered peptide that has A, G, or P at anchor position 2

Any altered peptide that has D, F, L, or Y at position 3

Any altered peptide that has E, G, L, N, Q, R, T, or V at position 4

Any altered peptide that has A, G, M, N, Q, R, K or V at position 5

Any altered peptide that has I, K, or T at position 6

Any altered peptide that has M or V at position 7

Any altered peptide that has I, L, M, or V at anchor position 9

Any altered peptide where deleterious residues at the following positions are replaced:

P1: P

P2: D, E, H, K, R

P9: D, E, F, G, H, K, N, P, Q, R, S, W, Y

#### **HLA-B\*5201 (8-mer peptides)**

Any altered peptide that has I, L, M, or V at position 1

Any altered peptide that has G, P, or Q at anchor position 2

Any altered peptide that has D, F, I, L, P, W, or Y at position 3

Any altered peptide that has A, E, I, K, L, P, or V at position 4

Any altered peptide that has A, F, G, I, L, M, T or V at position 5

Any altered peptide that has K, L, N, S or T at position 6

Any altered peptide that has E, K, Q, or Y at position 7

Any altered peptide that has F, I, L, M, or V at anchor position 8

Any altered peptide where deleterious residues at the following positions are replaced:

P1: P  
P2: H, K, R  
P3: R  
P8: D, E, G, H, K, N, P, Q, R, S

**HLA-B\*5801**

Any altered peptide that has I, K, or R at position 1  
Any altered peptide that has A, S, or T at anchor position 2  
Any altered peptide that has D at position 3  
Any altered peptide that has E, K, or P at position 4  
Any altered peptide that has F, I, L, M, or V at position 5  
Any altered peptide that has F, I, L, or V at position 6  
Any altered peptide that has L, M, N, or Y at position 7  
Any altered peptide that has K, N, R, or T at position 8  
Any altered peptide that has F, W, or Y at anchor position 9

Any altered peptide where deleterious residues at the following positions are replaced:

P1: D, E, P  
P2: D, E, F, H, I, K, L, M, N, Q, R, V, W, Y  
P9: D, E, G, H, K, N, P, Q, R, S

**HLA-B\*60**

Any altered peptide that has D or E at anchor position 2  
Any altered peptide that has A, I, L, M, S, or V at position 3  
Any altered peptide that has L, I, or V at position 5  
Any altered peptide that has I, L, M, V, or Y at position 7  
Any altered peptide that has K, Q, or R at position 8  
Any altered peptide that has I, L, M, or V at anchor position 9

Any altered peptide where deleterious residues at the following positions are replaced:

P1: P  
P2: F, H, I, K, L, M, Q, R, V, W, Y  
P9: D, E, F, G, H, K, N, P, Q, R, S, W, Y

**HLA-B\*61**

Any altered peptide that has G or R at position 1  
Any altered peptide that has D or E at anchor position 2  
Any altered peptide that has A, F, I, L, M, T, V, W, or Y at position 3  
Any altered peptide that has I at position 6  
Any altered peptide that has Y at position 7  
Any altered peptide that has A, I, L, M, or V at anchor position 9  
Any altered peptide where deleterious residues at the following positions are replaced:

P1: P  
P2: F, H, I, K, L, M, Q, R, V, W, Y  
P9: D, E, F, G, H, K, N, P, Q, R, S, W, Y

**HLA-B\*61 (8-mer peptides)**

Any altered peptide that has G or R at position 1  
Any altered peptide that has D or E at anchor position 2  
Any altered peptide that has A, F, I, L, M, T, V, W, or Y at position 3  
Any altered peptide that has I at position 6  
Any altered peptide that has Y at position 7  
Any altered peptide that has A, I, L, M, or V at anchor position 8  
Any altered peptide where deleterious residues at the following positions are replaced:

P1: P  
P2: F, H, I, K, L, M, Q, R, V, W, Y  
P8: D, E, F, G, H, K, N, P, Q, R, S, W, Y

**HLA-B\*62**

Any altered peptide that has I at position 1  
Any altered peptide that has I, L, Q at anchor position 2  
Any altered peptide that has G, K, R at position 3  
Any altered peptide that has D, E, G, or P at position 4  
Any altered peptide that has F, G, I, L, or V at position 5  
Any altered peptide that has I, L, T, V at position 6

Any altered peptide that has T, V, or Y at position 7

Any altered peptide that has F, W, Y at anchor position 9

Any altered peptide where deleterious residues at the following positions are replaced:

P1: P

P2: D, E, F, H, K, N, R, S, W, Y

P3: D, E

P6: D, E, K, R

P9: D, E, G, H, K, N, P, Q, R, S

#### **HLA-Cw0301**

Any altered peptide that has A or R at anchor position 2

Any altered peptide that has F, I, L, M, V, or Y at position 3

Any altered peptide that has E, P, or R at position 4

Any altered peptide that has N at position 5

Any altered peptide that has F, M, or Y at position 6

Any altered peptide that has K, M, R, or S at position 7

Any altered peptide that has T at position 8

Any altered peptide that has F, I, L, M at anchor position 9

Any altered peptide where deleterious residues at the following positions are replaced:

P1: P

P3: D, K, R

P6: D, E, K, R

P9: D, E, G, H, K, N, P, Q, R, S,

#### **HLA-Cw0401**

Any altered peptide that has F, P, W, or Y at anchor position 2

Any altered peptide that has D, or H at position 3

Any altered peptide that has D or E at position 4

Any altered peptide that has A, H, M, R, or T at position 5

Any altered peptide that has I, L, M, or V at position 6

Any altered peptide that has A at position 7

Any altered peptide that has H, K, or S at position 8

Examples of predicted human Class I MHC binding peptides – **continued**

Rank	Start Position	Subsequence	Score (estimated half time of dissociation)	<u>SEQ ID NO.</u>
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Any altered peptide that has F, I, L, M, V or Y at anchor position 9

Any altered peptide where deleterious residues at the following positions are replaced:

P1: P

P2: D, E, H, K, R

P9: D, E, G, H, K, N, P, Q, R, S

**HLA-Cw0602**

Any altered peptide that has F, I, K, or Y at position 1

Any altered peptide that has A, P, Q, or R at anchor position 2

Any altered peptide that has F, I, K, L, or M at position 5

Any altered peptide that has I, L, or V at position 6

Any altered peptide that has K, N, Q, or R at position 7

Any altered peptide that has I, L, M, V, or Y at anchor position 9

Any altered peptide where deleterious residues at the following positions are replaced:

P1: P

P9: D, E, G, H, K, N, P, Q, R, S

Examples of predicted human Class I MHC binding peptides from the C35 aa sequence and how they might be changed to improve binding:

**HLA-A\*0101**

Rank	Start Position	Subsequence	Score (estimated half time of dissociation)	<u>SEQ ID NO.</u>
1	77	KLENGGRPY	225.000	
2	16	EVEPGSGVR	90.000	
3	29	YCEPCGFEA	45.000	
4	39	YLELASAVK	36.000	
5	2	SGEPGQTSV	2.250	G is deleterious at P2

example of improved peptide    STEPGQTSV    22.50    G replaced with T @ P2    SEQ ID NO:85

Examples of predicted human Class I MHC binding peptides – **continued**

Rank	Start Position	Subsequence	Score (estimated half time of dissociation)	SEQ ID NO.
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example of improved peptide STEPGQISY **5625.00** **V at P9 replaced with Y, P7 enhanced** SEQ ID NO:86

**HLA-A\*0101 (10-mer peptides)**

1	66	EIEINGQLVF	45.000
2	16	EVEPGSGVRI	18.000
3	29	YCEPCGFEAT	9.000
4	26	VVEYCEPCGF	9.000
5	52	GIEIESRLGG	2.250

example of improved peptide GTEPSRLGY **1125.000** **replace I with T @P2  
replace G with Y @P9  
P5 enhanced with P** SEQ ID NO:87

**HLA-A\*0201 (9-mer peptides)**

1	9	SVAPPPEEV	2.982
2	104	KITNSRPPC	2.391
3	105	ITNSRPPCV	1.642
4	25	IVVEYCEPC	1.485
5	65	FEIEINGQL	1.018

example of improved peptide FLIEINWYL **16619.000** SEQ ID NO:88

**HLA-A\*0201 (10-mer peptides)**

1	58	RLGGTGAFEI	60.510
2	104	KITNSRPPCV	33.472
3	65	FEIEINGQLV	25.506
4	83	FPYEKDLIEA	4.502

P is deleterious at P2

example of improved peptide FLYEKDLIEA **689.606** **replace P with L @ P2** SEQ ID NO:89

Examples of predicted human Class I MHC binding peptides – **continued**

Rank	Start Position	Subsequence	Score (estimated half time of dissociation)	SEQ ID NO.
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example of improved peptide FLYEKDLIEW **9654.485** replace A with V @ P9 SEQ ID NO:90

5 33 CGFEATYLEL 3.173

**HLA-A\*0205**

1	65	FEIEINGQL	8.820	
2	25	IVVEYCEPC	3.060	
3	9	SVAPPPEEV	2.000	
4	104	KITNSRPPC	1.500	
5	81	GGFPYEKDL	1.260	G is deleterious at P2

example of improved peptide GVFPYEKDL **50.400** replace G with V @ P2 SEQ ID NO:91

**HLA-A\*0205 (10-mer peptides)**

1 33 CGEFATYLEL 6.300 G is deleterious at P2

example of improved peptide CVEFATYLEL **11.200** replace G with V @ P2 SEQ ID NO:92

2	104	KITNSRPPCV	6.000	
3	65	FEIEINGQLV	2.520	
4	53	IEIESRLGGT	1.428	
5	83	FPYEKDLIEA	1.350	P is deleterious at P2

example of improved peptide FVYEKDLIEA **54.000** replace P with V @ P2 SEQ ID NO:93

**HLA-A24**

1	34	GFEATYLEL	33.000	
2	49	QYPGIEIES	11.550	
example of improved peptide	QYPGIEIEL	<b>462.000</b>	enhance P9	<u>SEQ ID NO:94</u>
3	70	NGQLZFSKL	11.088	

Examples of predicted human Class I MHC binding peptides – **continued**

Rank	Start Position	Subsequence	Score (estimated half time of dissociation)	<u>SEQ ID NO.</u>
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4	38	TYLELASAV	10.800	
5	82	GFPYEKDLI	7.500	

**HLA-A24 (10-mer peptides)**

1	64	AFEIEINGQL	42.000	
2	74	VFSKLENGGF	10.000	
3	84	PYEKDLIEAI	9.000	
4	69	INGQLVFSKL	7.392	

example of improved peptide **IYGQLVFSKL 369.6** **enhance P2** **SEQ ID NO:95**

5	28	EYCEPCGFEA	6.600	
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**HLA-A3**

1	77	KLENGGFPY	36.000	
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example of improved peptide **KLENGGFPK 180.000** **enhance P9** **SEQ ID NO:96**

2	39	YLELASAVK	20.000	
3	101	TLEKITNSR	6.000	
4	61	GTGAFEIEI	0.540	
5	69	INGQLVFSK	0.360	<i>N is deleterious @ P2</i>

example of improved peptide **ILGQLVFSK 180.000** **replace N with L @ P2** **SEQ ID NO:97**

**HLA-A3 (10-mer peptides)**

1	68	EINGQLVFSK	8.100	
2	58	RLGGTGAFEI	2.700	
3	41	ELASAVKEQY	1.800	
4	78	LENGGFPYEK	0.810	<i>E is deleterious @ P2</i>

example of improved peptide **LLNGGFPYEK 270.000** **replace E with L @ P2** **SEQ ID NO:98**

Examples of predicted human Class I MHC binding peptides – c ntinued

Rank	Start Position	Subsequence	Score (estimated half time of dissociation)	<u>SEQ ID NO.</u>
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5	95	RASNGETLEK	0.400	
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**HLA- A\*1101**

1	39	YLELASAVK	0.400	
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2	69	INGQLVFSK	0.120	<i>N</i> is deleterious @ P2
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example of improved peptide    IVGQLVFSK    **6.000**    replace **N** with **V** @ P2    SEQ ID NO:99

3	16	EVEPGSGVR	0.120	
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4	101	TLEKITNSR	0.080	
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5	61	GTGAFEIEI	0.060	
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**HLA-A\*1101 (10-mer peptides)**

1	95	RASNGETLEK	1.200	
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2	38	TYLELASAVK	0.600	
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3	68	EINGGLVFSK	0.360	
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4	78	LENGGFPLYEK	0.120	<i>E</i> is deleterious @ P2
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example of improved peptide    LVNGGFPLYEK    **4.000**    replace **E** with **V** @ P2    SEQ ID NO:100

5	100	ETLEKITNSR	0.090	
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**HLA-A\*3101**

1	101	TLEKITNSR	2.000	
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2	16	EVEPGSGVR	0.600	
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3	50	YPGIEIESR	0.400	
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4	87	KDLIEAIRR	0.240	<i>D</i> is deleterious @ P2
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example of improved peptide    KILIEAIRR    **12.000**    replace **D** with **I** @ P2    SEQ ID NO:101

5	39	YLELASAVK	0.200	
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Examples of predicted human Class I MHC binding peptides – c ntinued

Rank	Start Position	Subsequence	Score (estimated half time of dissociation)	<u>SEQ ID NO.</u>
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**HLA-A\*3302**

1	16	EVEPGSGVR	45.000
2	101	TLEKITNSR	9.000
3	50	YPGIEIESR	3.000
4	66	EIEINGQLV	1.500
5	56	ESRLGGTGA	1.500

**HLA-A\*3302 (10-mer peptides)**

1	49	QYPGIEIESR	15.000
2	100	ETLEKITNSR	9.000
3	16	EVEPGSGVRI	1.500
4	28	EYCEPCGFEA	1.500
5	68	EINGQLVFSK	1.500

**HLA-A68.1**

1	16	EVEPGSGVR	900.000
2	9	SVAPPPEEV	12.000
3	50	YPGIEIESR	10.000

example of improved peptide    YVGIEIESR    400.000    enhance P2    SEQ ID NO:102

4	96	ASNGETLEK	9.000
5	101	TLEKITNSR	5.000

**HLA-A68.1 (10-mer peptides)**

1	100	ETLEKITNSR	300.000
2	16	EVEPGSGVRI	18.000
3	68	EINGGLVFSK	9.000
4	15	EEVEPGSGVR	9.000 <i>E is deleterious @ P2</i>

Examples of predicted human Class I MHC binding peptides – **continued**

Rank	Start Position	Subsequence	Score (estimated half time of dissociation)	SEQ ID NO.
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example of improved peptide EVVEPGSGR 1200.00 replace E with V @ P2 SEQ ID NO:103

5 95 RASNGETLEK 3.000

**HLA-B14**

1 94 RRASNGETL 20.000

2 57 SRLGGTGAF 5.000

example of improved peptide SRLGGTGAL 100.000 enhance P9 SEQ ID NO:104

3 100 ETLEKITNS 3.375

4 105 ITNSRPPCV 2.000

5 88 DLIEAIRRA 1.350

**HLA-B14 (10-mer peptides)**

1 103 EKITNSRPPC 6.750

example of improved peptide ERITNSRPPL 900.000 enhance P10 SEQ ID NO:105

2 33 CGFEATYLEL 5.000

3 93 IRRASNGETL 4.000

4 18 EPGSGVRIVV 3.000

5 88 DLIEAIRRAS 2.250

**HLA-B40**

1 65 FEIEINGQL 80.000

2 3 GEPGQTSVA 40.000

3 35 FEATYLELA 40.000

4 15 EEVEPGSGV 24.000

example of improved peptide EEVEPGSGL 120.000 enhance P9 SEQ ID NO:106

5 67 IEINGQLVF 16.000

Examples of predicted human Class I MHC binding peptides – **continued**

Rank	Start Position	Subsequence	Score (estimated half time of dissociation)	SEQ ID NO.
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**HLA-B40 (10-mer peptides)**

1	55	IESRLGGTGA	20.000	
2	53	IEIESRLGGT	16.000	
example of improved peptide		IEIESRLGGL	<b>80.000</b>	<b>enhance P10</b>
				<u>SEQ ID NO:107</u>
3	65	FEIEINGQLV	16.000	
4	67	IEINGQLVFS	16.000	
5	99	GETLEKITNS	8.000	

**HLA-B60**

1	65	FEIEFNGQL	387.200	
2	17	VEPGSGVRI	17.600	
example of improved peptide		VEPGSGVRL	<b>352.000</b>	<b>enhance P9</b>
				<u>SEQ ID NO:108</u>
3	15	EEVEPGSGV	16.000	
4	47	KEQYPGIEI	16.000	
5	85	YEKDLIEAI	8.800	

**HLA-B60 (10-mer peptides)**

1	65	FEIEINGQLV	16.000	
example of improved peptide		FEIEINGQLL	<b>320.000</b>	<b>enhance P10</b>
				<u>SEQ ID NO:109</u>
2	106	TNSRPPCVIL	16.000	
3	53	IEIESRLGGT	8.000	
4	33	CGFEATYLEL	8.000	
5	17	VEPGSGVRIV	8.000	

Examples of predicted human Class I MHC binding peptides – **continued**

Rank	Start Position	Subsequence	Score (estimated half time of dissociation)	SEQ ID NO.
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**HLA-B61**

1	15	EEVEPGSGV	80.000
2	35	FEATYLELA	40.000

example of improved peptide	FEATYLELV	<b>160.000</b>	enhance P9	<u>SEQ ID NO:110</u>
3	3	GEPGQTSVA	22.000	
4	65	FEIEINGQL	16.000	
5	85	YEKDLIEAI	16.000	

**HLA-B61 (10-mer peptides)**

1	65	FEIEINGQLV	80.000
2	17	VEPGSGVRI	40.000
3	55	IESRLGGTGA	20.000
4	87	KDLIEAIRRA	10.000

example of improved peptide	KELIEAIRRV	<b>160.000</b>	enhance P2, P10	<u>SEQ ID NO:111</u>
5	53	IEIESRLGGT	8.000	

**HLA-B62**

1	77	KLENGGF	24.000	
2	21	SGVRIVVEY	4.800	
3	75	FSKLENGGF	3.000	
4	31	EPCGFEATY	2.640	<i>P</i> is deleterious @ P2

example of improved peptide	EQCGFEATY	<b>105.6</b>	replace P with Q @ P2	<u>SEQ ID NO:112</u>
5	88	DLIEAIRRA	2.200	

Examples of predicted human Class I MHC binding peptides – c ntinued

Rank	Start Position	Subsequence	Score (estimated half time of dissociation)	SEQ ID NO.
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**HLA-B62 (10-mer peptides)**

1	41	ELASAVKEQY	40.000	
2	58	RLGGTGAFEI	9.600	
3	66	EIEINGQLVF	7.920	
4	56	ESRLGGTGAF	6.000	<i>S is deleterious @ P2</i>

example of improved peptide **EQRLGGTGAF 480.000** **replace S with Q @ P2** SEQ ID NO:113

5	20	GSGVRIVVEY	4.800	<i>S is deleterious @ P2</i>
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example of improved peptide **GQGVRIVVEY 384.000** **replace S with Q @P2** SEQ ID NO:114

**HLA-B7**

1	107	NSRPPCVIL	60.000	
example of improved peptide		NPRPPCVIL	<b>1200.000</b>	<b>enhance P2</b> <u>SEQ ID NO:115</u>
2	45	AVKEQYPGI	6.000	
3	22	GVRIVVEYC	5.000	
4	70	NGQLVFSKL	4.000	
5	81	GGFPYEKDL	4.000	

**HLA-B7 (10-mer peptides)**

1	50	YPGIEIESRL	80.000	
2	31	EPCGFEATYL	80.000	
3	18	EPGSGVRIVV	6.000	

example of improved peptide **EPGSGVRIVL 120.000** **enhance P10** SEQ ID NO:116

4	106	TNSRPPCVIL	6.000	
5	80	NGGFPYEKDL	4.000	

Examples of predicted human Class I MHC binding peptides – **continued**

Rank	Start Position	Subsequence	Score (estimated half time of dissociation)	SEQ ID NO.
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**HLA-B8**

1	107	NSRPPCVIL	4.000	
2	45	AVKEQYPGI	1.500	
3	105	ITNSRPPCV	0.600	
4	56	ESRLGGTGA	0.400	
5	100	ETLEKITNS	0.300	<i>S</i> is deleterious @ P9

example of improved peptide    ETLEKITNL    **12.000**    replace **S** with **L** @ **P9**    SEQ ID NO:117

**HLA-B8 (8-mer peptides)**

1	83	FPYEKDLI	6.000	
2	107	NSRPPCVI	1.000	
3	91	EAIRRAS <i>N</i>	0.800	<i>N</i> is deleterious @ P8

example of improved peptide    EAIRRASL    **32.000**    replace **N** with **L** @ **P9**    SEQ ID NO:118

4	20	GSGVRIVV	0.600	
5	18	EPGSGVRI	0.400	

**HLA-B8 (10-mer peptides)**

1	50	YPGIEIESRL	0.800	
2	93	IRRASNGETL	0.400	

example of improved peptide    IA RASNGETL    **16.000**    replace **R** with **A** @ **P2**    SEQ ID NO:119

3	31	EPCGFEATYL	0.320	
4	104	KITNSRPPCV	0.300	
5	18	EPGSGVRIVV	0.240	

Examples of predicted human Class I MHC binding peptides – c ntinued

Rank	Start Position	Subsequence	Score (estimated half time of dissociation)	<u>SEQ ID NO.</u>
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**HLA-B\*2702**

1	57	SRLGGTGAF	200.000
2	94	RRASNGETL	180.000

example of improved peptide	RRASNGETF	<b>600.000</b>	enhance P9	<u>SEQ ID NO:120</u>
3	93	IRRASNGET	20.000	
4	27	VEYCEPCGF	15.000	
5	77	KLENGGFY	9.000	

**HLA-B\*2702 (10-mer peptides)**

1	93	IRRASNGETL	60.000	
2	94	RRASNGETLE	6.000	
3	30	CEPCGFEATY	3.000	
4	58	RLGGTGAFEI	2.700	
5	23	VRIVVEYCEP	2.000	<i>P</i> is deleterious @ P10

example of improved peptide	VRIVVEYCEY	<b>200.000</b>	replace P with Y @ P10	<u>SEQ ID NO:121</u>
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**HLA-B\*2705**

1	94	RRASNGETL	6000.000
2	57	SRLGGTGAF	1000.000
3	93	IRRASNGET	200.000

example of improved peptide	IRRASNGEL	<b>2000.000</b>	enhance P9	<u>SEQ ID NO:122</u>
4	27	VEYCEPCGF	75.000	
5	77	KLENGGFY	45.000	

Examples of predicted human Class I MHC binding peptides – **continued**

Rank	Start Position	Subsequence	Score (estimated half time of dissociation)	<u>SEQ ID NO.</u>
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**HLA-B\*2705 (10-mer peptides)**

1	93	IRRASNGETL	2000.000	
2	94	RRASNGETLE	60.000	<i>E is deleterious @ P2</i>

example of improved peptide **RRASNGETLL 6000.000** **replace E with L @ P2** SEQ ID NO:123

3	78	LENGGF PYEK	30.000	
4	95	RASNGETLEK	30.000	
5	58	RLGGTGAFEI	27.000	

**HLA-B\*3501**

1	31	EPCGFEATY	40.000	
2	75	FSKLENGGF	22.500	

example of improved peptide **FPKLENGGM 120.000** **enhance P2, P9** SEQ ID NO:124

3	107	NSRPPCVIL	15.000	
4	42	LASAVKEQY	6.000	
5	18	EPGSGVRI	4.000	

**HLA-B\*3501 (10-mer peptides)**

1	31	EPCGFEATYL	30.000	
2	50	YPGIEIESRL	20.000	
3	56	ESRLGGTGAF	15.000	
4	20	GSGVRIVVEY	10.000	
5	83	FPYEKDLIEA	6.000	

example of improved peptide **FPYEKDLIEM 120.000** **enhance P10** SEQ ID NO:125

Examples of predicted human Class I MHC binding peptides – **continued**

Rank	Start Position	Subsequence	Score (estimated half time of dissociation)	<u>SEQ ID NO.</u>
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**HLA-B\*3701**

1	65	FEIEINGQL	15.000
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example of improved peptide **FDIEINGQL** **60.000** **enhance P2** SEQ ID NO:126

2	47	KEQYPGIEI	10.000
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3	85	YEKDLIEAI	10.000
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4	17	VEPGSGVRI	10.000
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5	35	FEATYLELA	5.000
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**HLA-B\*3701 (10-mer peptides)**

1	65	FEIEINGQLV	10.000
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example of improved peptide **FDIEINGQLI** **200.000** **enhance P2, P10** SEQ ID NO:127

2	67	IEINGQLVFS	5.000
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3	81	GGFPYEKDLI	5.000
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4	87	KDLIEAIRRA	4.000
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5	30	CEPCGFEATY	2.000
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**HLA-B\*3801**

1	34	GFEATYLEL	6.000
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example of improved peptide **GHEATYLEL** **90.000** **enhance P2** SEQ ID NO:128

2	70	NGQLVFSKL	1.560
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3	38	TYLELASAV	1.040
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4	81	GGFPYEKDL	1.000
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5	97	SNGETLEKI	0.720
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Examples of predicted human Class I MHC binding peptides – **continued**

Rank	Start Position	Subsequence	Score (estimated half time of dissociation)	<u>SEQ ID NO.</u>
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**HLA-B\*3801 (10-mer peptides)**

1	64	AFEIEINGQL	7.800
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example of improved peptide **AHEIEINGQL** **117.000** **enhance P2** SEQ ID NO:129

2	31	EPCGFEATYL	4.800
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3	66	EIEINGQLVF	3.000
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4	26	VVEYCEPCGF	3.000
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5	50	YPGIEIESRL	2.600
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**HLA-B\*3901**

1	94	RRASNGETL	15.000
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example of improved peptide **RHASNGETL** **90.000** **enhance P2** SEQ ID NO:130

2	34	GFEATYLEL	9.000
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3	38	TYLELASAV	4.000
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4	66	EIEINGQLV	3.000
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5	2	SGEPGQTSV	3.000
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**HLA-B\*3901 (10-mer peptides)**

1	33	CGFEATYLEL	12.000
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example of improved peptide **CHFEATYLEL** **360.000** **enhance P2** SEQ ID NO:131

2	64	AFEIEINGQL	9.000
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3	93	IRRASNGETL	4.500
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4	46	VKEQYPGIEI	3.000
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5	16	EVEPGSGVRI	3.000
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Examples of predicted human Class I MHC binding peptides – c ntinued

Rank	Start Position	Subsequence	Score (estimated half time of dissociation)	<u>SEQ ID NO.</u>
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**HLA-B\*3902**

1	70	NGQLVFSKL	2.400
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example of improved peptide **NKQLVFSKL** **24.000** **enhance P2** SEQ ID NO:132

2	81	GGFPYEKDL	2.400
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3	94	RRASNGETL	2.000
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4	34	GFEATYLEL	2.000
---	----	-----------	-------

5	107	NSRPPCVIL	0.600
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**HLA-B\*3902 (10-mer peptides)**

1	69	INGQLVFSKL	2.400
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2	64	AFEIEINGQL	2.400
---	----	------------	-------

3	50	YPGIEIESRL	2.400
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4	80	NGGFPYEKDL	2.400
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5	106	TNSRPPCVIL	2.000
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**HLA-B\*4403**

1	67	IEINGQLVF	200.000
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example of improved peptide **IEINGQLVY** **900.000** **enhance P9** SEQ ID NO:133

2	27	VEYCEPCGF	40.000
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3	21	SGVRIVVEY	36.000
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4	65	FEIEINGQL	20.000
---	----	-----------	--------

5	35	FEATYLELA	12.000
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Examples of predicted human Class I MHC binding peptides – **continued**

Rank	Start Position	Subsequence	Score (estimated half time of dissociation)	<u>SEQ ID NO.</u>
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**HLA-B\*4403 (10-mer peptides)**

1	30	CEPCGFEATY	120.000
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2	53	IEIESRLGGT	30.000
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example of improved peptide **IEIESRLGGY** **900.000** **enhance P10** SEQ ID NO:134

3	67	IEINGQLVFS	30.000
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4	65	FEIEINGQLV	20.000
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5	17	VEPGSGVRI	18.000
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**HLA-B\*5101**

1	18	EPGSGVRI	484.000
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2	59	LGGTGAF	114.400
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example of improved peptide **LPGTGAF** **572.000** **enhance P2** SEQ ID NO:135

3	2	SGEPGQTSV	48.400
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4	81	GGFPYEKDL	44.000
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5	70	NGQLVFSKL	22.000
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**HLA-B\*5101 (10-mer peptides)**

1	18	EPGSGVRI	440.000
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2	44	SAVKEQYPGI	220.000
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example of improved peptide **SPVKEQYPGI** **440.000** **enhance P2** SEQ ID NO:136

3	31	EPCGFEATYL	220.000
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4	81	GGFPYEKDLI	176.000
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5	50	YPGIEIESRL	157.300
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Examples of predicted human Class I MHC binding peptides – **continued**

Rank	Start Position	Subsequence	Score (estimated half time of dissociation)	<u>SEQ ID NO.</u>
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**HLA-B\*5102**

1	18	EPGSGVRI	242.000
2	81	GGFPYEKDL	110.000

example of improved peptide **GPFPYEKDI** **2200.000** **enhance P2, P9** SEQ ID NO:137

3	59	LGGTGAFEI	96.800
4	70	NGQLVFSKL	48.400
5	2	SGEPGQTSV	24.200

**HLA-B\*5102 (10-mer peptide)**

1	44	SAVKEQYPGI	726.000
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example of improved peptide **SPVKEQYPGI** **1452.000** **enhance P2** SEQ ID NO:138

2	50	YPGIEIESRL	400.000
3	81	GGFPYEKDLI	400.000
4	18	EPGSGVRIVV	220.000
5	31	EPCGFEATYL	121.000

**HLA-B\*5103**

1	59	LGGTGAFEI	48.400
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example of improved peptide **LAFTGAFEI** **145.200** **enhance P2** SEQ ID NO:139

2	2	SGEPGQTSV	44.000
3	18	EPGSGVRIV	44.000
4	70	NGQLVFSKL	7.260
5	81	GGFPYEKDL	7.200

Examples of predicted human Class I MHC binding peptides – **continued**  
Rank Start Subsequence Score

Position (estimated half time of dissociation) SEQ ID NO.

**HLA-B\*5103 (10-mer peptide)**

1	44	SAVKEQYPGI	110.000
2	81	GGFPYEKDLI	52.800
3	18	EPGSGVRIVV	44.000

example of improved peptide **EAGSGVRIVV 110.000** **enhance P2** SEQ ID NO:140

4	60	GGTGAFEIEI	44.000
5	33	CGFEATYLEL	7.920

**HLA-B\*5201**

1	18	WPGSGVRIV	75.000
2	67	LEINGQLVF	22.500

example of improved peptide **LQINGQLVI 450.000** **enhance P2, P9** SEQ ID NO:141

3	59	LGGTGAFEI	11.250
4	98	NGETLEKIT	11.000
5	19	PGSGVRIVV	10.000

**HLA-B\*5201 (10-mer peptides)**

1	18	EPGSGVRIVV	100.000
2	17	VEPGSGVRIV	45.000

example of improved peptide **VQPGSGVRIV 450.000** **enhance P2** SEQ ID NO:142

3	81	GGFPYEKDLI	33.000
4	105	ITNSRPPCVI	15.000
5	37	ATYLELASAV	12.000

Examples of predicted human Class I MHC binding peptides – **continued**

Rank	Start Position	Subsequence	Score (estimated half time of dissociation)	<u>SEQ ID NO.</u>
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**HLA-B\*5801**

1	75	FSKLENGGF	40.000	
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example of improved peptide    FSKLENGGW    **80.000**    **enhance P9**    SEQ ID NO:143

2	42	LASAVKEQY	4.500	
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3	107	NSRPPCVIL	4.000	
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4	61	GTGAFEIEI	3.000	
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5	105	ITNSRPPCV	3.000	
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**HLA-B\*5801 (10-mer peptides)**

1	56	ESRLGGTGAF	12.000	
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2	20	GSGVRIVVVEY	10.800	
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example of improved peptide    GSGVRIVVVEW    **144.000**    **enhance P10**    SEQ ID NO:144

3	1	MSGEPGQTSV	4.000	
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4	105	ITNSRPPCVI	3.000	
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5	37	ATYLELASAV	3.000	
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**HLA-Cw\*0301**

1	65	FEIEINGQL	30.000	
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2	81	GGFPYEKDL	18.000	
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3	70	NGQLVFSKL	12.000	
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4	57	SRLGGTGAF	10.000	
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5	34	GFEATYLEL	10.000	
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Examples of predicted human Class I MHC binding peptides – **continued**

Rank	Start Position	Subsequence	Score (estimated half time of dissociation)	<u>SEQ ID NO.</u>
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**HLA-Cw\*0301 (10-mer peptides)**

1	44	SAVKEQYPGI	50.000
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example of improved peptide    **SAVKEQYPGL 100.000**    **enhance P10**    SEQ ID NO:145

2	33	CGFEATYLEL	45.000
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3	69	INGQLVFSKL	12.000
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4	81	GGFPYEKDLI	3.750
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5	106	TNSRPPCVIL	3.000
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**HLA-Cw\*0401**

1	34	GFEATYLEL	240.000
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2	38	TYLELASAV	30.000
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3	82	GFPYEKDLI	25.000
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4	18	EPGSGVRI	20.000
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5	31	EPCGFEATY	12.000
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example of improved peptide    **EFCGFEATL 200.000**    **enhance P2, P9**    SEQ ID NO:146

**HLA-Cw\*0401 (10-mer peptides)**

1	64	AFEIEINGQL	200.000
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2	74	VFSKLENGGF	100.000
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example of improved peptide    **VFSKLENGGL 200.000**    **enhance P10**    SEQ ID NO:147

3	50	YPGIEIESRL	80.000
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4	31	EPCGFEATYL	80.000
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5	18	EPGSGVRIVV	10.000
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Examples of predicted human Class I MHC binding peptides – **continued**

Rank	Start Position	Subsequence	Score (estimated half time of dissociation)	SEQ ID NO.
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**HLA-Cw\*0602**

1	85	YEKDLIEAI	6.600
2	65	FEIEINGQL	6.600
3	21	SGVRIVVNEY	6.000
4	31	EPCGFEATY	3.300
5	61	GTGAGEIEI	3.000

**HLA-Cw\*0702**

1	31	EPCGFEATY	24.000
2	21	SGVRIVVNEY	19.200
3	42	LASAVKEQY	8.800
4	77	KLENGGF PY	4.000
5	49	QYPGIEIES	2.880

**HLA-Cw\*0702 (10-mer peptides)**

1	20	GSGVRIVVNEY	38.400
2	30	CEPCGFEATY	16.000
3	41	ELASAVKEQY	16.000
4	50	YPGIEIESRL	7.920
5	76	SKLENGGF PY	4.000